

(FILE 'HOME' ENTERED AT 13:18:28 ON 11 DEC 2007)

FILE 'REGISTRY' ENTERED AT 13:18:47 ON 11 DEC 2007

```
L1          9 S LSFAEPG/SQSP
L2        15032 S [LIMV]S[FWY][AGPST][ENDQ][PAGST][GAPST]/SQSP
L3        129 S L2 AND SQL<40
L4          4 S L2 AND SQL=13
L5          2 S L2 AND SQL=12
L6          4 S L2 AND SQL=11
L7        13 S L2 AND SQL=10
L8        10 S L2 AND SQL=9
L9          2 S L1 AND SQL=7
```

FILE 'HCAPLUS' ENTERED AT 13:21:56 ON 11 DEC 2007

```
L10         2 S L1 AND EPITOPE
```

=> s ;4

ENTER LOGIC EXPRESSION, QUERY NAME, OR (END):end
SEARCH ENDED BY USER

4 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l4 and epitope

```
      4 L4
      42073 EPITOPE
      43843 EPITOPES
      63788 EPITOPE
      (EPITOPE OR EPITOPES)
L11      2 L4 AND EPITOPE
```

=> s l5 and epitope

```
      2 L5
      42073 EPITOPE
      43843 EPITOPES
      63788 EPITOPE
      (EPITOPE OR EPITOPES)
L12      0 L5 AND EPITOPE
```

=> s l6 and epitope

```
      4 L6
      42073 EPITOPE
      43843 EPITOPES
      63788 EPITOPE
      (EPITOPE OR EPITOPES)
L13      2 L6 AND EPITOPE
```

=> s l7 and epitope

```
     15 L7
      42073 EPITOPE
      43843 EPITOPES
      63788 EPITOPE
      (EPITOPE OR EPITOPES)
L14     12 L7 AND EPITOPE
```

=> s l8 and epitope

```
     14 L8
      42073 EPITOPE
      43843 EPITOPES
      63788 EPITOPE
```

(EPI TOPE OR EPI TOPES)
L15 12 L8 AND EPI TOPE

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165336_us-10-510-875a-2.dx.rag.

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration, Ltd.
Run on: December 7, 2007, 23:02:13 : Search time 904 Seconds
(without alignments)
3.996 Million cell updates/sec

Title: US-10-510-875A-2
Perfect score: 13
Sequence: 1 XXRXS 6

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues
Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_200711.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000.*
4: Geneseqp2001.*
5: Geneseqp2002.*
6: Geneseqp2003a.*
7: Geneseqp2003b.*
8: Geneseqp2004a.*
9: Geneseqp2004b.*
10: Geneseqp2005.*
11: Geneseqp2006.*
12: Geneseqp2007.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	13	100.0	6	2	AAR48653	Aar48653 RGD conta
2	13	100.0	6	2	AAR72525	Aar72525 ADP-ribos
3	13	100.0	6	2	AAR72520	Aar72520 ADP-ribos
4	13	100.0	6	2	AAR70482	Aar70482 Cancer me
5	13	100.0	6	2	AAR98064	Aar98064 Peptide f
6	13	100.0	6	2	AAR22285	Aar22285 Urokinase
7	13	100.0	6	2	AAR34361	Aar34361 PKB subst
8	13	100.0	6	2	AAR56919	Aar56919 Enzyme in
9	13	100.0	6	2	AAR58834	Aar58834 Murine BA
10	13	100.0	6	2	AAR58836	Aar58836 Murine BA
11	13	100.0	6	2	AAR58840	Aar58840 Murine BA
12	13	100.0	6	2	AAR58842	Aar58842 Murine BA
13	13	100.0	6	2	AAR58838	Aar58838 Murine BA
14	13	100.0	6	2	AAR48766	Aar48766 Peptide f
15	13	100.0	6	2	AAR61330	Aar61330 BCL-XL/BC
16	13	100.0	6	2	AAR61326	Aar61326 BCL-XL/BC
17	13	100.0	6	2	AAR61324	Aar61324 BCL-XL/BC
18	13	100.0	6	2	AAR61328	Aar61328 BCL-XL/BC
19	13	100.0	6	2	AAR61332	Aar61332 BCL-XL/BC
20	13	100.0	6	2	AAR75357	Aar75357 Hexapepti
21	13	100.0	6	2	AAR75289	Aar75289 Hexapepti
22	13	100.0	6	2	AAR83868	Aar83868 Peptide s
23	13	100.0	6	2	AAR20434	Aar20434 Human mic
24	13	100.0	6	2	AAR20645	Aar20645 Human neu
25	13	100.0	6	2	AAR95206	Aar95206 Peptide f
26	13	100.0	6	2	AAR95201	Aar95201 Peptide f
27	13	100.0	6	2	AAR98886	Aar98886 Peptide S
28	13	100.0	6	2	ADH59030	Adh59030 GPIIb/III
29	13	100.0	6	2	ADE25445	Ade25445 GPIIb/III
30	13	100.0	6	2	AAR23392	Aar23392 V beta 6
31	13	100.0	6	2	AAR21734	Aar21734 Conserved
32	13	100.0	6	2	AAR27423	Aar27423 Human lac
33	13	100.0	6	2	AAR41791	Aar41791 ADP-ribos
34	13	100.0	6	2	AAR41796	Aar41796 ADP-ribos
35	13	100.0	6	2	AAR55251	Aar55251 ATCC HB 1
36	13	100.0	6	2	AAR43355	Aar43355 Pertussis
37	13	100.0	6	3	AAR50637	Aar50637 Alphas-pr
38	13	100.0	6	3	AAR54936	Aar54936 Peptide I
39	13	100.0	6	3	AAR58697	Aar58697 Human hae
40	13	100.0	6	3	AAR68345	Aar68345 Heat labi
41	13	100.0	6	3	AAR68340	Aar68340 Pertussis
42	13	100.0	6	3	AAR95263	Aar95263 Crostide
43	13	100.0	6	3	AAR93514	Aar93514 Peptide s
44	13	100.0	6	3	AAR22819	Aar22819 Human lac
45	13	100.0	6	3	AAR08371	Aar08371 Amino aci
46	13	100.0	6	4	AAR49566	Aar49566 Murine Va
47	13	100.0	6	4	AAR66214	Aar66214 B pertuss
48	13	100.0	6	4	AAR66219	Aar66219 E coli he
49	13	100.0	6	4	AAR67319	Aar67319 Peptide e
50	13	100.0	6	4	AAR67301	Aar67301 Peptide e

ALIGNMENTS

RESULT 1
ID AAR48653 standard; peptide; 6 AA.
XX AAR48653;
AC AAR48653;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1994 (first entry)

SCORE Search Results Details for Application 105108

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This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165341_us-1

GenCore version 6.2.1
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DM protein - protein search, using sw model
Run on: December 7, 2007, 23:05:54 ; Search time 16 Seconds
(without alignments)
35.738 Million cell updates/sec

Title: US-10-510-875A-2
Perfect score: 13
Sequence: 1 XXRXS 6
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
1	13	100.0	neural cell adhesi
2	13	100.0	hypothetical pepti
3	13	100.0	olfactory receptor
4	13	100.0	neuropeptide Grb-A
5	13	100.0	T-cell receptor ga
6	13	100.0	Ig heavy chain CRD
7	13	100.0	Ig heavy chain CRD
8	13	100.0	Ig H chain V-D-J r
9	13	100.0	T-cell receptor ga
10	13	100.0	T-cell receptor ga
11	13	100.0	TCR gamma V-J regi

12	13	100.0	11	2	A26120	6-phosphofructokin
13	13	100.0	12	2	PT0228	Ig heavy chain CDR
14	13	100.0	12	2	PH1611	Ig H chain V-D-J r
15	13	100.0	12	2	B39690	neural cell adhesi
16	13	100.0	12	2	S43170	kinesin light chai
17	13	100.0	12	2	A44874	proboscipedia - fr
18	13	100.0	12	2	S32472	lynnadPamide 2 - g
19	13	100.0	13	2	S32475	lynnadPamide 5 - g
20	13	100.0	13	2	S03879	6-phosphofructokin
21	13	100.0	13	2	S03879	DEB-A protein - fr
22	13	100.0	14	2	S38307	spermadhesin AWN h
23	13	100.0	14	2	S58426	Ig H chain V-D-J r
24	13	100.0	14	2	PH1597	Km(r) protein - Es
25	13	100.0	14	2	I56388	cathepsin L (EC 3.
26	13	100.0	14	2	S45655	hemocyanin chain 3
27	13	100.0	14	2	G61308	hypothetical prote
28	13	100.0	14	4	S00843	alpha-conotoxin GI
29	13	100.0	15	1	NTKNAG	ubiquinol-cytochro
30	13	100.0	15	2	S42741	heterogeneous ribo
31	13	100.0	15	2	A38304	T-cell receptor be
32	13	100.0	15	2	G49255	T-cell receptor be
33	13	100.0	15	2	B49655	T-cell receptor de
34	13	100.0	15	2	G35141	complement factor
35	13	100.0	15	2	PL0109	carbon-monoxide de
36	13	100.0	15	2	PL0143	modulation protein
37	13	100.0	15	2	S21411	GTP-binding protei
38	13	100.0	15	2	T03000	fumarate hydratase
39	13	100.0	15	2	PA0062	juvenile-hormone e
40	13	100.0	15	2	A36527	beaded-chain filam
41	13	100.0	15	2	A32921	ubiquinol-cytochro
42	13	100.0	15	2	FU0025	hypothetical prote
43	13	100.0	16	2	S51610	retinol-binding pr
44	13	100.0	16	2	B35491	Ig heavy chain CDR
45	13	100.0	16	2	PT0224	T cell receptor al
46	13	100.0	16	2	PH1771	T-cell receptor al
47	13	100.0	16	2	F41299	T-cell receptor be
48	13	100.0	16	2	PH0137	Ig H chain V-D-J r
49	13	100.0	16	2	PH1588	hypothetical prote
50	13	100.0	16	2	S30384	zinc finger protei

ALIGNMENTS

RESULT 1

A39690
neural cell adhesion molecule, cardiac splice form -,.-, - - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: A39690
R:Reyes, A.A.; Small, S.J.; Akeson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expre
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: A39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-7 <REY>
A:Cross-references: UNIPARC:UPI000017C964; GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 100.0%; Score 13; DB 2; Length 7;
Best Local Similarity 33.3%; Pred.No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510-875a-2.dx.rup.

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GenCore version 6.2.1
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JM protein - protein search, using sw model
Run on: December 7, 2007, 23:04:20 ; Search time 128 Seconds
(without alignments)
77.206 Million cell updates/sec

Title: US-10-510-875A-2
Perfect score: 13
Sequence: 1 XRRXXS 6
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5
Searched: 5032670 seqs, 1645091341 residues
Total number of hits satisfying chosen parameters: 5032670
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Uniprot_12.1.*
1: uniprot_sprot.*
2: uniprot_trembl.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Query Match %	ID	Description
1	13 100.0	8 1 UH09_RAT	P56575 rattus norv
2	13 100.0	8 2 A0N9W0_HUMAN	A0N9W0 homo sapien
3	13 100.0	8 2 Q80WDS_MUSSP	Q80WDS mus spretus
4	13 100.0	8 2 Q9QVJ8_HMURI	Q9QVJ8 mus sp. mep
5	13 100.0	8 2 O89965_POVJC	O89965 jc polyomav
6	13 100.0	8 2 Q6PUD7_SV40	Q6PUD7 simian viru
7	13 100.0	8 2 Q6QXS9_SV40	Q6QXS9 simian viru
8	13 100.0	8 2 Q6PUD5_SV40	Q6PUD5 simian viru

9	13 100.0	8 2 Q6PUD9_SV40	Q6PUD9 simian viru
10	13 100.0	8 2 Q6PUE1_SV40	Q6PUE1 simian viru
11	13 100.0	8 2 Q94VA7_9SAUR	Q94VA7 varanus sal
12	13 100.0	8 2 Q94VB2_9SAUR	Q94VB2 varanus sal
13	13 100.0	8 2 Q94VB5_9SAUR	Q94VB5 varanus sal
14	13 100.0	8 2 Q94VB8_9SAUR	Q94VB8 varanus yuw
15	13 100.0	9 2 Q7M3N7_GRYBI	Q7M3N7 gryllus bim
16	13 100.0	9 2 Q85V64_EUCGR	Q85V64 eucalyptus
17	13 100.0	9 2 Q91BM8_9POLY	Q91BM8 simian viru
18	13 100.0	9 2 Q9PYK1_9POLY	Q9PYK1 simian viru
19	13 100.0	9 2 Q94V10_VARGI	Q94V10 varanus gig
20	13 100.0	9 2 Q75QC9_GALLA	Q75QC9 gallus lafa
21	13 100.0	9 2 Q94VC6_9SAUR	Q94VC6 varanus pil
22	13 100.0	9 2 Q15SR6_CHICK	Q15SR6 gallus gall
23	13 100.0	10 1 AKHX_LOCHI	P81626 locusta mig
24	13 100.0	10 2 Q7R2Z2_NEUCR	Q7R2Z2 neurospora
25	13 100.0	10 2 Q7SA62_NEUCR	Q7SA62 neurospora
26	13 100.0	10 2 Q5SAQ0_HUMAN	Q5SAQ0 homo sapien
27	13 100.0	10 2 Q9TWX1_DERFA	Q9TWX1 dermatophag
28	13 100.0	10 2 Q3YAH8_MACMU	Q3YAH8 macaca mula
29	13 100.0	10 2 Q85V67_EUCGR	Q85V67 eucalyptus
30	13 100.0	10 2 Q9XMB4_AEGTA	Q9XMB4 aegilops ta
31	13 100.0	10 2 Q85BV5_EUCGR	Q85BV5 eucalyptus
32	13 100.0	10 2 Q85BV6_EUCGR	Q85BV6 eucalyptus
33	13 100.0	10 2 Q85BV7_EUCGR	Q85BV7 eucalyptus
34	13 100.0	10 2 Q9QVF1_9MURI	Q9QVF1 mus sp. pro
35	13 100.0	10 2 Q53X33_POVBK	Q53X33 bk polyomav
36	13 100.0	10 2 Q76V79_9POLY	Q76V79 polyomaviru
37	13 100.0	10 2 Q53X11_POVBK	Q53X11 bk polyomav
38	13 100.0	10 2 Q53X10_POVBK	Q53X10 bk polyomav
39	13 100.0	10 2 Q53X32_POVBK	Q53X32 bk polyomav
40	13 100.0	10 2 Q6X061_9SAUR	Q6X061 anolis haet
41	13 100.0	10 2 Q94VG5_9SAUR	Q94VG5 varanus gri
42	13 100.0	10 2 Q94VDS_VAROL	Q94VDS varanus oli
43	13 100.0	11 1 EFG_BACCE	P83067 bacillus ce
44	13 100.0	11 2 Q7S183_NEUCR	Q7S183 neurospora
45	13 100.0	11 2 Q29831_HUMAN	Q29831 homo sapien
46	13 100.0	11 2 Q5FBX0_HUMAN	Q5FBX0 homo sapien
47	13 100.0	11 2 Q7MAJ2_ASCSU	Q7MAJ2 ascaris suu
48	13 100.0	11 2 Q35374_PARTE	Q35374 paramedum
49	13 100.0	11 2 Q4YTE6_PLABE	Q4YTE6 plasmodium
50	13 100.0	11 2 Q7RMD3_PLAYO	Q7RMD3 plasmodium

ALIGNMENTS

RESULT 1			
UH09_RAT	UH09_RAT	Reviewed;	8 AA.
AC	P56575;		
DT	15-DEC-1998, integrated into UniprotKB/Swiss-Prot.		
DT	15-DEC-1998, sequence version 1.		
DT	24-JUL-2007, entry version 20.		
DT	Unknown protein from 2D-PAGE of heart tissue (Spot P9) (Fragment).		
JS	Rattus norvegicus (rat).		
JC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
JC	Muroidea; Muridae; Murinae; Rattus.		
DX	NCBI_TaxID=10116;		
RN	(1)		
RP	PROTEIN SEQUENCE.		
RC	STRAIN=Wistar; TISSUE=Heart;		
RA	Li X.-P., Fleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,		
RA	Jungblut P.R.;		

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165415_us-10-510-875a-6.rag.

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
JM protein - protein search, using sw model
Run on: December 7, 2007, 23:10:56 ; Search time 119 Seconds
(without alignments)
35.405 Million cell updates/sec

Title: US-10-510-875A-6
Perfect score: 36
Sequence: 1 LSFAPFG 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 3405708 seqs, 601879884 residues
Total number of hits satisfying chosen parameters: 3405708
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A Geneseq_200711:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000:*
4: Geneseqp2001:*
5: Geneseqp2002:*
6: Geneseqp2003a:*
7: Geneseqp2003b:*
8: Geneseqp2004a:*
9: Geneseqp2004b:*
10: Geneseqp2005:*
11: Geneseqp2006:*
12: Geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	36	100.0	7	7	ADES0785	Ades0785 Protein k
2	36	100.0	10	7	ADES0782	Ades0782 Protein k
3	36	100.0	10	7	ADES0786	Ades0786 Protein k
4	36	100.0	10	7	ADES0781	Ades0781 Protein k
5	36	100.0	10	7	ADES0789	Ades0789 Protein k
6	36	100.0	10	12	AEJ53756	Aej53756 Kinase no
7	36	100.0	10	12	AFB67165	Afb67165 Substrate
8	36	100.0	11	7	ADES0790	Ades0790 Protein k
9	36	100.0	11	7	ADES0787	Ades0787 Protein k
10	36	100.0	11	7	ADES0788	Ades0788 Protein k
11	36	100.0	11	12	AFH55968	Afh55968 Serine/Th
12	36	100.0	11	12	AFH55989	Afh55989 Serine/Th
13	36	100.0	13	7	ADES0791	Ades0791 Protein k
14	36	100.0	13	12	AFB67160	Afb67160 Substrate
15	33	91.7	189	10	AEH36370	Aeh36370 L. pneumo
16	33	91.7	189	10	AEH39786	Aeh39786 L. pneumo
17	33	91.7	484	4	AAE76522	Aab76522 Corynebac
18	33	91.7	491	4	AB45789	Aab45789 C. glutam
19	33	91.7	491	4	ADG90675	Aag90675 C. glutam
20	33	91.7	491	6	ADL65551	Adl65551 C. glutam
21	32	88.9	8	5	AAE23344	Aae23344 Human GSK
22	32	88.9	11	5	AAE23345	Aae23345 Human GSK
23	32	88.9	11	11	AEF22422	Aef22422 Fluoresce
24	32	88.9	11	11	AEH34583	Aeg34583 Akt1 assa
25	32	88.9	13	6	ABP54023	Abp54023 Akt speci
26	32	88.9	13	6	ABP54026	Abp54026 Akt speci
27	32	88.9	13	6	AAE29760	Aae29760 Akt speci
28	32	88.9	13	6	AAE79642	Aag79642 Human Akt
29	32	88.9	13	6	AB999474	Abb99474 Amino aci
30	32	88.9	13	7	AA024278	Aao24278 Akt pepti
31	32	88.9	13	7	ADG96165	Adg96165 Biotin la
32	32	88.9	13	7	ADE06653	Adel5867 Peptide s
33	32	88.9	13	7	ADL15867	Adel5867 Peptide s
34	32	88.9	13	7	ADK82126	Adk82126 Akt pepti
35	32	88.9	13	8	AD033600	Ado33600 Biotinyla
36	32	88.9	13	8	AD035205	Ado35205 Human Akt
37	32	88.9	13	8	ADU48697	Adu48697 Akt pepti
38	32	88.9	13	8	ADU48583	Adu48583 Akt pepti
39	32	88.9	13	8	ADU48747	Adu48747 Akt pepti
40	32	88.9	13	8	ADU48568	Adu48568 Akt pepti
41	32	88.9	13	10	AED60288	Aed60288 Akt pepti
42	32	88.9	13	11	AEJ27504	Aee27504 CHK1sv1 k
43	32	88.9	13	11	AEI19201	Aee19201 AKT subst
44	32	88.9	13	11	AEI44991	Aei44991 GSK3 [alph
45	32	88.9	13	11	AEI67776	Aei67776 Human Akt
46	32	88.9	13	11	AEJ15815	Aej15815 Checkpoin
47	32	88.9	13	11	AEJ15056	Aej15056 Human CHK
48	32	88.9	13	11	AEJ08095	Aej08095 Peptide s
49	32	88.9	13	11	AEK42820	Aek42820 Akt pepti
50	32	88.9	13	12	AEI43685	Aei43685 Human Akt

ALIGNMENTS

RESULT 1
ADES0785
ID ADES0785 standard; peptide; 7 AA.
XX
AC ADES0785;
XX
DT 29-JAN-2004 (first entry)
XX

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165420_us-10-510-875a-6.rup.

Score_Home_Page Retrieve Application List SCORE_System_Overview SCORE_FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165420_us-10-510-875a-6.rup.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
CM protein - protein search, using sw model
Run on: December 7, 2007, 23:11:41 ; Search time 653 Seconds
(without alignments)
17.635 Million cell updates/sec

Title: US-10-510-875A-6
Perfect score: 36
Sequence: 1 LSFAPFG 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Uniprot_12.1.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	372	A4BN04_9GAMM	A4bn04 nitrococcus
2	34	94.4	107	Q9IE13_9HIV2	Q9ie13 human immun
3	34	94.4	107	Q9IDV8_9HIV2	Q9idv8 human immun
4	34	94.4	107	Q9IE11_9HIV2	Q9ie11 human immun
5	34	94.4	107	Q9Q2M0_9HIV2	Q9q2m0 human immun
6	34	94.4	107	Q9IE09_9HIV2	Q9ie09 human immun
7	34	94.4	388	A3PQR3_RHO51	A3pqr3 rhodobacter
8	34	94.4	399	A6C8X3_9PLAN	A6c8x3 planctomyce

SUMMARIES

9	33	91.7	105	2	Q7YWS9_CABEL	Q7yws9 caenorhabdi
10	33	91.7	153	2	Q0SE94_AERPE	Q0se94 aeropyrum p
11	33	91.7	189	2	ASIEA3_LEGPC	Asiea3 legionella
12	33	91.7	189	2	Q5WUE4_LEGPL	Q5wue4 legionella
13	33	91.7	189	2	Q5X2Y4_LEGPL	Q5x2y4 legionella
14	33	91.7	189	2	Q5ZT60_LEGPL	Q5zt60 legionella
15	33	91.7	204	2	Q1FL69_CLOTR	Q1fl69 clostridium
16	33	91.7	223	2	Q9R284_DEIRA	Q9r284 deinococcus
17	33	91.7	282	2	Q21WF6_RHOED	Q21wf6 rhodoferax
18	33	91.7	391	2	Q8PFV4_XANAC	Q8pfv4 xanthomonas
19	33	91.7	420	2	Q2JFD4_FRASC	Q2jfd4 frankia sp.
20	33	91.7	429	2	Q0LM38_HERAU	Q0lm38 herpetosiph
21	33	91.7	484	2	Q6MEV5_CORGL	Q6mev5 corynebacte
22	33	91.7	491	2	Q93KF1_CORGL	Q93kf1 corynebacte
23	33	91.7	513	2	A0RS19_MYCS2	A0rs19 mycobacteri
24	33	91.7	516	2	A4QCH2_CORGB	A4qch2 corynebacte
25	33	91.7	807	2	Q57WE2_9TRYF	Q57we2 trypanosoma
26	33	91.7	886	2	Q8KAY9_CHLTE	Q8kay9 chlorobium
27	33	91.7	952	2	Q1GDN7_HALMD	Q1egn7 haloquadrat
28	33	91.7	958	2	Q3W9P2_9ACTO	Q3w9p2 frankia sp.
29	33	91.7	1113	2	Q3WIK6_9ACTO	Q3wik6 frankia sp.
30	33	91.7	2019	2	A6G178_9DELT	A6g178 plesiocysti
31	32	88.9	77	2	Q7UYI6_RHOBA	Q7uyi6 rhodopirell
32	32	88.9	161	2	Q4HIM3_9BACT	Q4him3 uncultured
33	32	88.9	161	2	Q4HIM6_9BACT	Q4him6 uncultured
34	32	88.9	161	2	Q4HIM2_9BACT	Q4him2 uncultured
35	32	88.9	161	2	Q4HIM4_9BACT	Q4him4 uncultured
36	32	88.9	161	2	Q4HIQ1_9BACT	Q4hiq1 uncultured
37	32	88.9	161	2	Q4HIM5_9BACT	Q4him5 uncultured
38	32	88.9	161	2	Q4HIM7_9BACT	Q4him7 uncultured
39	32	88.9	161	2	Q4HIM6_9BACT	Q4him6 uncultured
40	32	88.9	166	2	A4Q742_MAGGR	A4qc42 magnaporthi
41	32	88.9	197	2	A2ZJ15_ORYSI	A2zj15 oryza sativ
42	32	88.9	215	2	AIWF10_VEREI	AIwpi0 verinephro
43	32	88.9	233	1	TNFA_DRINU	Q1wm27 dasypus nov
44	32	88.9	233	1	TNFA_TRIVU	P79374 trichosurus
45	32	88.9	235	2	Q5W9H9_MERUN	Q5w9h9 meriones un
46	32	88.9	237	1	NFI_XANAC	Q8pim0 xanthomonas
47	32	88.9	237	2	Q3BR52_XANCS	Q3br52 xanthomonas
48	32	88.9	239	2	Q2PSR1_XANOC	Q2psr1 xanthomonas
49	32	88.9	259	2	Q91910_9NUCL	Q91910 culex nigri
50	32	88.9	266	2	Q5DHL3_SCHJA	Q5dhl3 schistosoma

ALIGNMENTS

RESULT 1
A4BN04_9GAMM
ID A4BN04_9GAMM
AC A4BN04_9GAMM
Unreviewed; 372 AA.
DT 03-APR-2007, integrated into UniprotKB/TREMBL.
DT 03-APR-2007, sequence version 1.
DT 24-JUL-2007, entry version 3.
DE Putative dehydrogenase protein.
EN ORFNames=NB231_09133;
DS Nitrococcus mobilis Nb-231.
JC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
JC Ecotiorhodospiraceae; Nitrococcus.
CX NCBI_TaxID=314278;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nb-231;
RA Waterbury J., Ferriera S., Johnson J., Kravitz S., Halpern A.,
RA Remington K., Beeson K., Tran B., Rogers Y.-H., Friedman R.,

RA Venter J.C.;
RL Submitted (FEB-2006) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAOF01000002; EAK22603.1; -; Genomic_DNA.
DR InterPro: IPR012938; GSDH.
DR Pfam; PF07995; GSDH; 1.
PE 4: Predicted;
SQ SEQUENCE 372 AA; 40153 MW; 7522FCAA6A526171 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LSFAEPG 7
DB 110 LSFAEPG 116

RESULT 2
291E13_9HIV2 Unreviewed; 107 AA.
AC Q91E13;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 24-JUL-2007, entry version 28.
DE Envelope glycoprotein gp105 (Fragment).
EN Name=env;
CS Human immunodeficiency virus 2.
CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
CC Lentivirus; Primate lentivirus group.
CX NCBI_TaxID=11709;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20414625; PubMed=10957727; DOI=10.1089/08892220050117069;
RA Parreira R., Esteves A., Santos C., Piedade J., Venenno T.,
RA Canas-Ferreira W.F.;
RT *Genetic variability of human immunodeficiency virus type 2 C2V3
RT region within and between individuals from Bissau, Guinea-Bissau, West
RT Africa.*;
RL AIDS Res. Hum. Retroviruses 16:1307-1312(2000).
CC -----
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CC -----
DR EMBL; AJ246915; CAB95067.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA:InterPro.
DR InterPro: IPR000777; GP120.
DR Gene3D; G3DSA:2.170.40.20; GP120; 1.
DR Pfam; PF00516; GP120; 1.
PE 4: Predicted;
KW Envelope protein.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12550 MW; C6FBAF65E9FB66B25 CRC64;

Query Match 94.4%; Score 34; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LSFAEPG 7
DB 110 LSFAEPG 116

RESULT 3
291D18_9HIV2 Unreviewed; 107 AA.
AC Q91D18;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 24-JUL-2007, entry version 27.
DE Envelope glycoprotein gp105 (Fragment).
EN Name=env;
CS Human immunodeficiency virus 2.
CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
CC Lentivirus; Primate lentivirus group.
CX NCBI_TaxID=11709;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20414625; PubMed=10957727; DOI=10.1089/08892220050117069;
RA Parreira R., Esteves A., Santos C., Piedade J., Venenno T.,
RA Canas-Ferreira W.F.;
RT *Genetic variability of human immunodeficiency virus type 2 C2V3
RT region within and between individuals from Bissau, Guinea-Bissau, West
RT Africa.*;
RL AIDS Res. Hum. Retroviruses 16:1307-1312(2000).
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CC -----
DR EMBL; AJ246915; CAB95092.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA:InterPro.
DR InterPro: IPR000777; GP120.
DR Gene3D; G3DSA:2.170.40.20; GP120; 1.
DR Pfam; PF00516; GP120; 1.
PE 4: Predicted;
KW Envelope protein.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12578 MW; C06D9DA7EC3BCB32 CRC64;

Query Match 94.4%; Score 34; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LSFAEPG 7
DB 94 ISFAEPG 100

RESULT 4
291E11_9HIV2 Unreviewed; 107 AA.
AC Q91E11;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 24-JUL-2007, entry version 28.
DE Envelope glycoprotein gp105 (Fragment).
EN Name=env;
CS Human immunodeficiency virus 2.
CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
CC Lentivirus; Primate lentivirus group.
CX NCBI_TaxID=11709;

2Y 1 LSFAEPG 7
DB 94 ISFAEPG 100

RESULT 3
291D18_9HIV2 Unreviewed; 107 AA.
AC Q91D18;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 24-JUL-2007, entry version 27.
DE Envelope glycoprotein gp105 (Fragment).
EN Name=env;
CS Human immunodeficiency virus 2.
CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
CC Lentivirus; Primate lentivirus group.
CX NCBI_TaxID=11709;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20414625; PubMed=10957727; DOI=10.1089/08892220050117069;
RA Parreira R., Esteves A., Santos C., Piedade J., Venenno T.,
RA Canas-Ferreira W.F.;
RT *Genetic variability of human immunodeficiency virus type 2 C2V3
RT region within and between individuals from Bissau, Guinea-Bissau, West
RT Africa.*;
RL AIDS Res. Hum. Retroviruses 16:1307-1312(2000).
CC -----
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CC -----
DR EMBL; AJ246915; CAB95092.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA:InterPro.
DR InterPro: IPR000777; GP120.
DR Gene3D; G3DSA:2.170.40.20; GP120; 1.
DR Pfam; PF00516; GP120; 1.
PE 4: Predicted;
KW Envelope protein.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12578 MW; C06D9DA7EC3BCB32 CRC64;

Query Match 94.4%; Score 34; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LSFAEPG 7
DB 94 ISFAEPG 100

RESULT 4
291E11_9HIV2 Unreviewed; 107 AA.
AC Q91E11;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 24-JUL-2007, entry version 28.
DE Envelope glycoprotein gp105 (Fragment).
EN Name=env;
CS Human immunodeficiency virus 2.
CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
CC Lentivirus; Primate lentivirus group.
CX NCBI_TaxID=11709;

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165425_us-1

GenCore version 6.2.1
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Run on: December 7, 2007, 23:12:02 ; Search time 39 Seconds
(without alignments)
17.270 Million cell updates/sec

Title: US-10-510-875A-6
Perfect score: 36
Sequence: 1 LSPAFPG 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	91.7	223	2 H75600	hypothetical prote
2	32	88.9	124	2 S16870	protein kinase (EC
3	32	88.9	483	1 TVRTKA	protein kinase (EC
4	31	86.1	623	2 T02007	ABCl protein homol
5	31	86.1	623	2 T52128	hypothetical prote
6	31	86.1	2195	2 T34264	hypothetical prote
7	30	83.3	259	1 ONGAOL	ovulation hormone
8	30	83.3	360	2 S52662	adenosylmethionine
9	30	83.3	373	2 B70819	probable carnitine
10	30	83.3	478	2 A37430	calcitonin recepto
11	30	83.3	479	2 S33746	calcitonin recepto

12	30	83.3	485	2 E83620	probable amidase P
13	30	83.3	485	2 T41714	hypothetical serin
14	30	83.3	515	2 T60800	calcitonin recepto
15	30	83.3	535	2 S65762	chitinase (EC 3.2.
16	30	83.3	727	2 T23585	hypothetical prote
17	30	83.3	946	2 F84280	ATP-dependent heli
18	30	83.3	1108	2 T35827	probable membrane
19	30	83.3	2175	1 GNNYBE	genome polyprotein
20	30	83.3	2214	1 A48548	hypothetical prote
21	29	80.6	134	2 G72713	hypothetical prote
22	29	80.6	258	2 T21959	hypothetical prote
23	29	80.6	262	2 G70001	acetyl-CoA carboxy
24	29	80.6	276	2 T08773	hypothetical prote
25	29	80.6	282	2 F84045	acetyl-CoA carboxy
26	29	80.6	294	2 AE1271	acetyl-CoA carboxy
27	29	80.6	294	2 AG1633	acetyl-CoA carboxy
28	29	80.6	305	2 T06020	transcription fact
29	29	80.6	330	2 AH1859	hypothetical prote
30	29	80.6	427	2 S71367	UI snRNP 70K prote
31	29	80.6	431	2 JC7730	1-aminocyclopropan
32	29	80.6	515	2 G70806	probable acetolact
33	29	80.6	515	2 S72987	acetolactate synth
34	29	80.6	614	2 T23790	hypothetical prote
35	29	80.6	617	2 T49059	hypothetical prote
36	29	80.6	699	2 T09069	probable cAMP-resp
37	29	80.6	786	2 I49274	mammary gland fact
38	29	80.6	793	2 S54772	mammary gland fact
39	29	80.6	794	2 G02317	transcription acti
40	29	80.6	794	2 S55527	mammary gland fact
41	29	80.6	821	2 E87503	1,4-beta-D-glucan
42	29	80.6	823	2 B87348	1,4-beta-D-glucan
43	29	80.6	942	2 C96574	hypothetical prote
44	29	80.6	980	2 T00045	celloextrin phosph
45	29	80.6	1515	2 A40203	4-alpha-glucanotra
46	29	80.6	1555	2 S38758	amylo-alpha-1,6-gl
47	29	80.6	2254	2 T09053	low voltage-activa
48	28	77.8	112	2 B43431	phosphorylase kina
49	28	77.8	139	2 S30850	hypothetical prote
50	28	77.8	185	2 E75311	hypothetical prote

ALIGNMENTS

RESULT 1

H75600
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75600
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.;
Science 286, 1571-1577, 1999
A:title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; PMID:20036896; PMID:10567266
A:Accession: H75600
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-223 <WHI>
A:CROSS-references: UNIPROT:Q9RZ84; UNIPARC:UPI00000C1610; GB:AE001825; GB:AE001862; GB:AE001825; GB:AE001825; I
C:Genetics:
A:Gene: DRA0070
A:Map position: 2

Query Match 91.7% Score 33; DB 2; Length 223;

Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2y 1 LSFAPFG 7
|:|||||
Db 198 LAFAPFG 204

RESULT 2

S16870

protein kinase (EC 2.7.1.37) GSK-3-alpha - rabbit (fragments)

N/Alternate names: factor A; glycogen synthase kinase 3 alpha

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-1995

C/Accession: S16870

R/Woodgett, J.R.

EMBO J. 9, 2431-2438, 1990

A/Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.

A/Reference number: S14707; MUID:90316097; PMID:2164470

A/Accession: S16870

A/Molecule type: protein

A/Residues: 1-124 <MO>

A/Cross-references: UNIPROT:U000017557A

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:39-92/Domain: protein kinase homology (fragments) <KIN>

Query Match 88.9%; Score 32; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 2 SFAEPFG 7

|||||

Db 3 SFAEPFG 8

RESULT 3

IVRTKA

protein kinase (EC 2.7.1.37) GSK-3-alpha - rat

N/Alternate names: factor A; glycogen synthase kinase 3 alpha

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C/Accession: S14707

R/Woodgett, J.R.

EMBO J. 9, 2431-2438, 1990

A/Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.

A/Reference number: S14707; MUID:90316097; PMID:2164470

A/Accession: S14707

A/Molecule type: mRNA

A/Residues: 1-483 <MO>

A/Cross-references: UNIPROT:P18265; UNIPARC:UPT000012DDBF; EMBL:X53427; NID:956331; PIDN:CAA37518.1;

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F:117-378/Domain: protein kinase homology <KIN>

F:125-133/Region: protein kinase ATP-binding motif

F:148/Active site: Lys #status predicted

Query Match 88.9%; Score 32; DB 1; Length 483;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 2 SFAEPFG 7

|||||

Db 21 SFAEPFG 26

RESULT 4

T02007

ABC1 protein homolog T15B16.14 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C/Accession: T02007

R/Stoneking, T.; Smith, R.

Submitted to the EMBL Data Library, November 1998

A/Description: The sequence of A. thaliana T15B16.

A/Reference number: Z14488

A/Accession: T02007

A/Status: translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-623 <STO>

A/Cross-references: UNIPROT:Q9SBB2; UNIPARC:UPI00000A3E05; EMBL:AF104919; NID:93859590; PID:93859601

A/Experimental source: Cultivar Columbia

C/Genetics:

A/Map position: 4

A/Introns: 182/2; 257/3; 308/3; 361/3; 415/1; 490/3

A/Note: T15B16.14

Query Match 86.1%; Score 31; DB 2; Length 623;

Best Local Similarity 85.7%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1 LSFAPFG 7

|||||

Db 533 LFPAPFG 539

RESULT 5

T52128

ABC1 protein homolog [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52128

R/Dujardin, G.

Submitted to the EMBL Data Library, December 1997

A/Reference number: Z25969

A/Accession: T52128

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-623 <DUJ>

A/Cross-references: UNIPROT:O65576; UNIPARC:UPI00000A25AB; EMBL:AJ001158; PIDN:CAA04557.1

A/Experimental source: ecotype Columbia; seedling

C/Genetics:

A/Note: ABC1A

Query Match 86.1%; Score 31; DB 2; Length 623;

Best Local Similarity 85.7%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1 LSFAPFG 7

|||||

Db 533 LFPAPFG 539

RESULT 6

T34264

hypothetical protein F46C8.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C/Accession: T34264

R/Wilcox, L.

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165336_us-10-510-875a-7.dx.rag.

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CM protein - protein search, using sw model
Run on: December 7, 2007, 23:02:13 ; Search time 1054 Seconds
(without alignments)
3.996 Million cell updates/sec

Title: US-10-510-875A-7
Perfect score: 33
Sequence: 1 LXPAPPG 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues
Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

- Database :
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000.*
 - 4: Geneseqp2001.*
 - 5: Geneseqp2002.*
 - 6: Geneseqp2003a.*
 - 7: Geneseqp2003b.*
 - 8: Geneseqp2004a.*
 - 9: Geneseqp2004b.*
 - 10: Geneseqp2005.*
 - 11: Geneseqp2006.*
 - 12: Geneseqp2007.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ‡ Query

No.	Score	Match	Length	DB	ID	Description
1	33	100.0	7	7	ADES0785	Ade50785 Protein k
2	33	100.0	10	7	ADES0782	Ade50782 Protein k
3	33	100.0	10	7	ADES0786	Ade50786 Protein k
4	33	100.0	10	7	ADES0781	Ade50781 Protein k
5	33	100.0	10	7	ADES0789	Ade50789 Protein k
6	33	100.0	10	12	AEN53756	Aen53756 Kinase no
7	33	100.0	10	12	AFB67165	Afb67165 Substrate
8	33	100.0	11	7	ADES0790	Ade50790 Protein k
9	33	100.0	11	7	ADES0787	Ade50787 Protein k
10	33	100.0	11	7	ADES0788	Ade50788 Protein k
11	33	100.0	11	12	AFH55968	Afh55968 Serine/Th
12	33	100.0	11	12	AFH55989	Afh55989 Serine/Th
13	33	100.0	13	7	ADES0791	Ade50791 Protein k
14	33	100.0	13	12	AFB67160	Afb67160 Substrate
15	33	100.0	98	4	AAU54359	Aau54359 Propionib
16	33	100.0	98	6	ABM50878	Abm50878 Propionib
17	33	100.0	296	10	ABM93500	Abm93500 M. xanthu
18	33	100.0	345	8	AFR46133	Afr46133 Recombina
19	33	100.0	420	8	ADX77623	Adx77623 Plant ful
20	33	100.0	426	8	ADY12256	Ady12256 Plant ful
21	33	100.0	426	8	ADX78935	Adx78935 Plant ful
22	33	100.0	484	4	AA376522	Aab76522 Corynebac
23	33	100.0	491	4	AA345789	Aab45789 C. glutam
24	33	100.0	491	4	AAG90675	Aag90675 C. glutam
25	33	100.0	491	6	ADL65551	Adl65551 C. glutam
26	33	100.0	832	7	ABO76120	Abo76120 Pseudomon
27	33	100.0	1864	2	AAW22602	Aaw22602 Tyllactone
28	31	93.9	404	10	AEC95873	Aec95873 Goldfish
29	31	93.9	450	10	ABM92976	Abm92976 M. xanthu
30	31	93.9	1089	5	ADF91892	Adf91892 Agarase I
31	31	93.9	2195	8	ADN24175	Adn24175 Bacterial
32	30	90.9	53	5	ABP10072	Abp10072 Human ORF
33	30	90.9	68	4	ABB64040	Abb64040 Drosophil
34	30	90.9	68	4	ABB69113	Abb69113 Drosophil
35	30	90.9	68	10	AFCI4089	Afc14089 Fruit fly
36	30	90.9	68	10	AFB98869	Afb98869 Fruit fly
37	30	90.9	146	7	ABO70246	Abo70246 Pseudomon
38	30	90.9	146	8	ADX96708	Adx96708 plant ful
39	30	90.9	189	10	AEB36370	Aeb36370 L. pneumo
40	30	90.9	189	10	AEB39786	Aeb39786 L. pneumo
41	30	90.9	197	8	ABOS8613	Abos8613 Human gen
42	30	90.9	289	4	AAG90376	Aag90376 C. glutam
43	30	90.9	294	6	ADD13210	Add13210 C. glutam
44	30	90.9	344	8	ADR86501	Adr86501 Aspergill
45	30	90.9	353	4	ABG17211	Abg17211 Novel hum
46	30	90.9	382	6	ABM86018	Abm86018 Rice abio
47	30	90.9	416	8	ADN21187	Adn21187 Bacterial
48	30	90.9	430	11	AES88756	Aes88756 S. agalac
49	30	90.9	430	11	AES93498	Aes93498 S. agalac
50	30	90.9	430	11	AES84218	Aes84218 S. agalac

ALIGNMENTS

RESULT 1
ADES0785
ID ADES0785 standard; peptide; 7 AA.
XX ADES0785;
AC ADES0785;
XX 29-JAN-2004 (first entry)
DT
XX

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This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165341_us-1

GenCore version 6.2.1
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3M protein - protein search, using sw model
Run on: December 7, 2007, 23:05:54 ; Search time 19 Seconds
(without alignments)
35.738 Million cell updates/sec

Title: US-10-510-875A-7
Perfect score: 33
Sequence: 1 LXFAPFG 7
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result NO.	Score	Query Match	Length	DB ID	Description
1	33	100.0	223	2 H75600	hypothetical prote
2	33	100.0	623	2 T02007	ABCI protein homol
3	33	100.0	623	2 T52128	ABCI protein homol
4	31	93.9	2175	1 GNYBYE	genome polypeptide
5	31	93.9	2195	2 T34264	hypothetical prote
6	31	93.9	2214	1 A48548	genome polypeptide
7	30	90.9	139	2 S30850	hypothetical prote
8	30	90.9	256	2 T00097	probable carnitine
9	30	90.9	373	2 B70819	hypothetical prote
10	30	90.9	383	2 T39854	calcitonin recepto
11	30	90.9	478	2 A37430	

12	30	90.9	479	2 S33746	calcitonin recepto
13	30	90.9	515	2 I60800	calcitonin recepto
14	30	90.9	617	2 T49059	hypothetical prote
15	30	90.9	699	2 T09069	probable cAMP-resp
16	30	90.9	874	2 S25530	glycoprotein B - b
17	30	90.9	946	2 F84280	ATP-dependent heli
18	30	90.9	1108	2 T35827	probable membrane
19	29	87.9	124	2 S16870	protein kinase (EC
20	29	87.9	185	2 E75311	hypothetical prote
21	29	87.9	225	2 E87468	Surf1 family prote
22	29	87.9	258	2 T21959	hypothetical prote
23	29	87.9	262	2 G70001	acetyl-CoA carboxy
24	29	87.9	272	2 S58127	seed albumin - mun
25	29	87.9	276	2 T08773	hypothetical prote
26	29	87.9	277	1 A45961	2,5-diketo-D-gluc
27	29	87.9	282	2 F84045	acetyl-CoA carboxy
28	29	87.9	294	2 AE1271	acetyl-CoA carboxy
29	29	87.9	294	2 AG1633	transcription regu
30	29	87.9	299	2 E81035	probable lysR-fami
31	29	87.9	299	2 E81979	conserved hypotet
32	29	87.9	313	2 H69984	hypothetical prote
33	29	87.9	341	2 C82161	ferric enterobacti
34	29	87.9	347	2 A75265	threonine synthase
35	29	87.9	352	1 DMFKTG	threonine synthase
36	29	87.9	352	2 A25364	probable men - My
37	29	87.9	362	2 A70547	hypothetical prote
38	29	87.9	379	2 A83404	metabolite transpo
39	29	87.9	427	2 E90371	UL snRNP 70K prote
40	29	87.9	427	2 S71367	hypothetical prote
41	29	87.9	435	2 D72379	conserved hypotet
42	29	87.9	467	2 E75395	protein kinase (EC
43	29	87.9	483	1 TVRTKA	1-aminocyclopropan
44	29	87.9	488	2 T47943	conserved hypotet
45	29	87.9	490	2 F87443	probable acetolact
46	29	87.9	515	2 G70806	acetolactate synth
47	29	87.9	515	2 S72987	hypothetical prote
48	29	87.9	614	2 T23790	hemocyanin chain a
49	29	87.9	631	1 BHTLA	hypothetical glyci
50	29	87.9	767	2 E70895	

ALIGNMENTS

RESULT 1

H75600
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75600
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.;
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75600
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <WHI>
A;Cross-references: UNIPROT:Q9R284; UNIPARC:UPI00000C1610; GB:AE001862; GB:AE001825; NID:96460468; I
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0070
A;Map position: 2

Query Match 100.0%; score 33; DB 2; Length 223;

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510-875a-7.dx.rup.

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3M protein - protein search, using sw model
Run on: December 7, 2007, 23:04:20 ; Search time 149 Seconds
(without alignments)
77.206 Million cell updates/sec

Title: US-10-510-875A-7
Perfect score: 33
Sequence: 1 LXPAPPG 7
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5
Searched: 5032670 seqs, 1645091341 residues
Total number of hits satisfying chosen parameters: 5032670
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Uniprot_12.1.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match %	Description
1	33	100.0	80 2 Q5LM62_SILPO
2	33	100.0	105 2 Q7TW59_CAEL
3	33	100.0	161 2 Q4HIM3_9BACT
4	33	100.0	161 2 Q4HIM6_9BACT
5	33	100.0	161 2 Q4HIM2_9BACT
6	33	100.0	161 2 Q4HIM4_9BACT
7	33	100.0	161 2 Q4H101_9BACT
8	33	100.0	161 2 Q4HIM5_9BACT

9	33	100.0	161 2 Q4HIM7_9BACT
10	33	100.0	161 2 Q4HIM6_9BACT
11	33	100.0	197 2 A2ZJ15_ORYSI
12	33	100.0	213 2 A6GK3_9BELT
13	33	100.0	223 2 Q9R284_DEIRA
14	33	100.0	233 1 TNFA_DSNO
15	33	100.0	233 1 TNFA_TRIUV
16	33	100.0	235 2 Q5W9H9_MERUN
17	33	100.0	236 2 A6GY31_FLALPJ
18	33	100.0	248 2 Q8S302_FLALPJ
19	33	100.0	254 2 A5FNC0_CVTJ0
20	33	100.0	264 2 Q0LDD4_HERAU
21	33	100.0	288 2 Q131Y3_BURXL
22	33	100.0	304 2 A4ISF3_GEOTN
23	33	100.0	304 2 Q5KVN9_GEOKA
24	33	100.0	315 2 Q5P4G9_AZOSE
25	33	100.0	318 2 Q7F9D9_ORYSJ
26	33	100.0	322 2 Q650M6_ORYSJ
27	33	100.0	324 2 Q5LRP8_SILPO
28	33	100.0	337 2 Q0K120_RALEH
29	33	100.0	338 2 Q46TC5_RALEJ
30	33	100.0	351 2 A2XTV0_ORYSI
31	33	100.0	351 2 Q7X8Q0_ORYSJ
32	33	100.0	372 2 A4BN04_9GNMM
33	33	100.0	388 2 A4AERO_9ACTN
34	33	100.0	400 2 A4U1L7_9PROT
35	33	100.0	410 2 A3BJ48_ORYSJ
36	33	100.0	415 2 Q1DBF2_MYXND
37	33	100.0	420 2 Q2JFD4_FRASC
38	33	100.0	421 2 Q0JCY3_ORYSJ
39	33	100.0	429 2 Q0LM38_HERAU
40	33	100.0	466 2 Q26VZ4_XANP2
41	33	100.0	484 2 Q6M6V5_CORGL
42	33	100.0	491 2 Q93KF1_CORGL
43	33	100.0	513 2 Q0RS19_MVCS2
44	33	100.0	516 2 A4QCH2_CORGB
45	33	100.0	615 2 A3TUR5_9RHOB
46	33	100.0	623 2 Q65576_ARATH
47	33	100.0	623 2 Q9SBB2_ARATH
48	33	100.0	627 2 Q0BY76_HYPNA
49	33	100.0	644 2 A0T012_9VIRU
50	33	100.0	653 2 Q1GNQ1_SPHAL

ALIGNMENTS

RESULT 1	Q5LM62_SILPO	Unreviewed;	80 AA.
ID	Q5LM62_SILPO		
AC	Q5LM62;		
DT	01-FEB-2005, integrated into UniprotKB/TREMBL.		
DT	01-FEB-2005, sequence version 1.		
DT	24-JUL-2007, entry version 10.		
DE	Putative uncharacterized protein.		
SN	OrderedLocusNames=SPO3702;		
SC	Silicibacter pomeroyi.		
CC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;		
CC	Rhodobacteraceae; Silicibacter.		
DX	NCBI_TaxId=89184;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RC	STRAIN=ATCC 700808 / DSM 15171 / DSS-3;		
RX	PubMed=15602564; DOI=10.1038/nature03170;		
RA	Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,		

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165347_us-10-510-875a-2.dx.ra1.

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Run on: December 7, 2007, 23:06:38 ; Search time 88 Seconds
(without alignments)
9.719 Million cell updates/sec

Title: US-10-510-875A-2
Perfect score: 13
Sequence: 1 XXXXXS 6

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues
Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

- Database :
- 1: /EMC_Celerra_SIDS2/ptodata/1/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SIDS2/ptodata/1/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SIDS2/ptodata/1/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SIDS2/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /EMC_Celerra_SIDS2/ptodata/1/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SIDS2/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
1	13	100.0	6 1 US-08-039-786-2 Sequence 2, Appli
2	13	100.0	6 1 US-07-859-291C-19 Sequence 19, Appl
3	13	100.0	6 1 US-07-781-590A-5 Sequence 5, Appli

4	13	100.0	6 1 US-07-781-590A-9 Sequence 9, Appli
5	13	100.0	6 1 US-07-828-450-37 Sequence 37, Appl
6	13	100.0	6 1 US-08-082-847-13 Sequence 13, Appl
7	13	100.0	6 1 US-08-081-539-110 Sequence 110, App
8	13	100.0	6 1 US-08-466-647-110 Sequence 110, App
9	13	100.0	6 1 US-08-238-379-2 Sequence 2, Appli
10	13	100.0	6 1 US-07-942-157A-1 Sequence 1, Appli
11	13	100.0	6 1 US-08-259-569-4 Sequence 4, Appli
12	13	100.0	6 1 US-08-482-880-9 Sequence 9, Appli
13	13	100.0	6 1 US-08-273-274-9 Sequence 9, Appli
14	13	100.0	6 1 US-08-292-968-1 Sequence 1, Appli
15	13	100.0	6 1 US-08-292-968-6 Sequence 6, Appli
16	13	100.0	6 1 US-08-733-505A-3 Sequence 3, Appli
17	13	100.0	6 1 US-08-733-505A-5 Sequence 5, Appli
18	13	100.0	6 1 US-08-733-505A-9 Sequence 9, Appli
19	13	100.0	6 1 US-08-826-885-4 Sequence 4, Appli
20	13	100.0	6 1 US-08-480-229C-13 Sequence 13, Appl
21	13	100.0	6 1 US-08-659-235C-13 Sequence 13, Appl
22	13	100.0	6 1 US-08-475-041-9 Sequence 9, Appli
23	13	100.0	6 1 US-08-387-942C-12 Sequence 12, Appl
24	13	100.0	6 1 US-08-537-400-21 Sequence 21, Appl
25	13	100.0	6 1 US-08-467-974-1 Sequence 1, Appli
26	13	100.0	6 1 US-08-467-974-6 Sequence 6, Appli
27	13	100.0	6 1 US-08-484-773-9 Sequence 9, Appli
28	13	100.0	6 1 US-08-482-228-145 Sequence 145, App
29	13	100.0	6 1 US-08-361-864-13 Sequence 13, Appl
30	13	100.0	6 1 US-08-467-536-1 Sequence 1, Appli
31	13	100.0	6 1 US-08-467-536-6 Sequence 6, Appli
32	13	100.0	6 1 US-09-127-574-17 Sequence 17, Appl
33	13	100.0	6 2 US-08-482-528-145 Sequence 145, App
34	13	100.0	6 2 US-08-467-976-1 Sequence 1, Appli
35	13	100.0	6 2 US-08-467-976-6 Sequence 6, Appli
36	13	100.0	6 2 US-08-278-251-9 Sequence 9, Appli
37	13	100.0	6 2 US-08-478-140B-7 Sequence 7, Appli
38	13	100.0	6 2 US-09-082-514-1 Sequence 1, Appli
39	13	100.0	6 2 US-09-082-514-6 Sequence 6, Appli
40	13	100.0	6 2 US-09-177-249-50 Sequence 50, Appl
41	13	100.0	6 2 US-09-257-218-17 Sequence 17, Appl
42	13	100.0	6 2 US-09-311-760-17 Sequence 17, Appl
43	13	100.0	6 2 US-09-561-756-54 Sequence 54, Appl
44	13	100.0	6 2 US-09-338-943-7 Sequence 7, Appli
45	13	100.0	6 2 US-09-227-721-54 Sequence 54, Appl
46	13	100.0	6 2 US-09-155-613A-58 Sequence 58, Appl
47	13	100.0	6 2 US-08-865-579-17 Sequence 17, Appl
48	13	100.0	6 2 US-08-171-384A-6 Sequence 6, Appli
49	13	100.0	6 2 US-10-059-749-17 Sequence 17, Appl
50	13	100.0	6 2 US-09-954-697-54 Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-08-039-786-2
; Sequence 2, Application US/08039786
; Patent No. 5356784
; GENERAL INFORMATION:
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: DETERMINATION OF CONCENTRATION BY
; TITLE OF INVENTION: AFFINITY TITRATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.